SEQUENCE LISTING

<110>   Fung, Yuen Kai
         Gomer, Charles
         Ang, Anne T'

<120>   Methods To Enhance And Confine Expression of Genes

<130>   D6087D

<140>   10/051,345
<141>   2002-01-18
<150>   60/096,947
<151>   1998-08-18

<160>   9

<210>   1
<211>   441
<212>   DNA
<213>   Unknown

<220>

<221>   exon
<223>   sequence encoding N-terminus (amino acids 1-147)
         DNA-binding domain of yeast GAL4 protein

<400>   1
atgaagctac tgtcttctat cgaacaagca tgcgatattt gccgacttaa   50
aaagctcaag tgctccaaag aaaaaccgaa gtgcgccaag tgtctgaaga   100
acaactggga gtgtcgctac tctcccaaaa ccaaaaggtc tccgctgact   150
agggcacatc tgacagaagt ggaatcaagg ctagaaagac tggaacagct   200
atttctactg attttttcctc gagaagacct tgacatgatt ttgaaaatgg   250
attctttaca ggatataaaa gcattgttaa caggattatt tgtacaagat   300
aatgtgaata aagatgccgt cacagataga ttggcttcag tggagactga   350
tatgcctcta acattgagac agcatagaat aagtgcgaca tcatcatcgg   400
aagagagtag taacaaaggt caaagacagt tgactgtatc g   441

<210>   2
<211>   315
<212>   DNA
<213>   Unknown

<220>

<221>   exon
<223>   sequence encoding basic helix-loop-helix leucine
         zipper domain of Max (amino acids 8-112)

<400>   2
gaggtggaga gcgacgaaga gcaaccgagg tttcaatctg cggctgacaa   50

SEQ 1

```
acgggctcat cataatgcac tggaacgaaa acgtagggac cacatcaaag    100
acagctttca cagtttgcgg gactcagtcc catcactcca aggagagaag    150
gcatcccggg cccaaatcct agacaaagcc acagagtata tccagtatat    200
gcgaaggaaa aaccacacac accagcaaga tattgacgac ctcaagcggc    250
agaatgctct tctggagcag caagtccgtg cactggagaa ggcgaggtca    300
agtgcccaac tgcag                                         315


        <210>       3
        <211>       33
        <212>       DNA
        <213>       Unknown

        <220>

        <221>       exon
        <223>       sequence encoding the first 11 amino acids of Gal4

        <400>       3
atgaagctac tgtcttctat cgaacaagca tgc             33

        <210>       4
        <211>       387
        <212>       DNA
        <213>       Unknown

        <220>

        <221>       exon
        <223>       sequence encoding the C-terminus transactivation
                    domain of herpes simplex viral protein VP16

        <400>       4
gcgtacagcc gcgcgcgtac gaaaaacaat tacgggtcta ccatcgaggg    50
cctgctcgat ctcccggacg acgacgcccc cgaagaggcg gggctggcgg    100
ctccgcgcct gtcctttctc cccgcgggac acacgcgcag actgtcgacg    150
gcccccccga ccgatgtcag cctggggggac gagctccact tagacggcga    200
ggacgtggcg atggcgcatg ccgacgcgct agacgatttc gatctggaca    250
tgttggggga cggggattcc ccgggtccgg gatttacccc ccacgactcc    300
gcccctacg gcgctctgga tatggccgac ttcgagtttg agcagatgtt    350
taccgatgcc cttggaattg acgagtacgg tgggtag             387

        <210>       5
        <211>       270
        <212>       DNA
        <213>       Unknown

        <220>

        <221>       exon
        <223>       sequence encoding the basic helix-loop-helix
                    leucine zipper domain of c-Myc
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SEQ 2

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        <400>        5
accgaggaga atgtcaagag gcgaacacac aacgtcttgg agcgccagag    50
gaggaacgag ctaaaacgga gcttttttgc cctgcgtgac cagatcccgg   100
agttggaaaa caatgaaaag gcccccaagg tagttatcct taaaaaagcc   150
acagcataca tcctgtccgt ccaagcagag gagcaaaagc tcatttctga   200
agaggacttg ttgcggaaac gacgagaaca gttgaaacac aaacttgaac   250
agctacggaa ctcttgtgcg                                     270


        <210>        6
        <211>        17
        <212>        DNA
        <213>        Unknown

        <220>

        <221>        protein_bind
        <223>        a 17-mer DNA-binding site for Gal4

        <400>        6
cggaggactg tcctccg            17


        <210>        7
        <211>        1008
        <212>        DNA
        <213>        Unknown

        <220>

        <221>        misc_feature
        <223>        TET-ON sequence

        <400>        7
atgtctagat tagataaaag taaagtgatt aacagcgcat tagagctgct    50
taatgaggtc ggaatcgaag gtttaacaac ccgtaaactc gcccagaagc   100
ttggtgtaga gcagcctaca ctgtattggc atgtaaaaaa taagcgggct   150
ttgctcgacg ccttagccat tgagatgtta gataggcacc atactcactt   200
ttgccctttt aaaggggaaa gctggcaaga ttttttacgc aataacgcta   250
aaagttttag atgtgcttta ctaagtcatc gcaatggagc aaaagtacat   300
tcagatacac ggcctacaga aaaacagtat gaaactctcg aaaatcaatt   350
agcctttttta tgccaacaag gtttttcact agagaacgcg ttatatgcac   400
tcagcgctgt ggggcatttt actttaggtt gcgtattgga agatcaagag   450
catcaagtcg ctaaagaaga aagggaaaca cctactactg atagtatgcc   500
gccattatta cgacaagcta tcgaattatt tgatcaccaa ggtgcagagc   550
cagccttctt attcggcctt gaattgatca tatgcggatt agaaaaacaa   600
cttaaatgtg aaagtgggtc cgcgtacagc cgcgcgcgta cgaaaaacaa   650
ttacgggtct accatcgagg gcctgctcga tctcccggac gacgacgccc   700
ccgaagaggc ggggctggcg gctccgcgcc tgtcctttct ccccgcggga   750
cacacgcgca gactgtcgac ggcccccccg accgatgtca gcctggggga   800
cgagctccac ttagacggcg aggacgtggc gatggcgcat gccgacgcgc   850
tagacgattt cgatctggac atgttggggg acggggattc cccgggtccg   900
ggatttaccc cccacgactc cgcccctac ggcgctctgg atatggccga   950
cttcgagttt gagcagatgt ttaccgatgc ccttggaatt gacgagtacg  1000
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SEQ 3

gtgggtag   1008

<pre>
    <210>   8
    <211>   80
    <212>   DNA
    <213>   Unknown

    <220>

    <221>   misc_feature
    <223>   the first 80 bases of TET-ON sequence

    <400>   8
atgtctagat tagataaaag taaagtgatt aacagcgcat tagagctgct 50
taatgaggtc ggaatcgaag gtttaacaac   80

    <210>   9
    <211>   621
    <212>   DNA
    <213>   Unknown

    <220>

    <221>   exon
    <223>   sequence encoding tet repressor (amino acids 1-207)

    <400>   9
atgtctagat tagataaaag taaagtgatt aacagcgcat tagagctgct 50
taatgaggtc ggaatcgaag gtttaacaac ccgtaaactc gcccagaagc 100
ttggtgtaga gcagcctaca ctgtattggc atgtaaaaaa taagcgggct 150
ttgctcgacg ccttagccat tgagatgtta gataggcacc atactcactt 200
ttgcccttta aaaggggaaa gctggcaaga ttttttacgc aataacgcta 250
aaagttttag atgtgcttta ctaagtcatc gcaatggagc aaaagtacat 300
tcagatacac ggcctacaga aaaacagtat gaaactctcg aaaatcaatt 350
agccttttta tgccaacaag gtttttcact agagaacgcg ttatatgcac 400
tcagcgctgt ggggcatttt actttaggtt gcgtattgga agatcaagag 450
catcaagtcg ctaaagaaga aagggaaaca cctactactg atagtatgcc 500
gccattatta cgacaagcta tcgaattatt tgatcaccaa ggtgcagagc 550
cagccttctt attcggcctt gaattgatca tatgcggatt agaaaaacaa 600
cttaaatgtg aaagtgggtc c   621
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                        SEQ 4